

Db 421 tttgacttcgatttcagtttaggttggtgaatttttcaggttcocatttgtagccttt 480
Qy 481 agagcttgagcttcctccatgttaattccttgatcgaattctctagagaaaagggaag 540
Db 481 agagcttgagcttcctccatgttaattccttgatcgaattctctagagaaaagggaag 540
Qy 541 tgcattctgagttattgaaatcgagtgacatttttttttcaacgtgtccaatcaatcca 600
Db 541 tgcattctgagttattgaaatcgagtgacatttttttttcaacgtgtccaatcaatcca 600
Qy 601 caaaacaaagcagaacaggttaattcttcatactactactacagaaagtaagtcttaccg 660
Db 601 caaaacaaagcagaacaggttaattcttcatactactactacagaaagtaagtcttaccg 660
Qy 661 tcatgataataacgtctcgttcttcctcaagagggttttccgacatccataaacgaccca 720
Db 661 tcatgataataacgtctcgttcttcctcaagagggttttccgacatccataaacgaccca 720
Qy 721 agcctcatgaagcattaggaagacatttggcttctcttgatgagcctttataggtg 780
Db 721 agcctcatgaagcattaggaagacatttggcttctcttgatgagcctttataggtg 780
Qy 781 tcagcggagctgcgaattcccgctccgactggctccgcaaaatattcgaacggcaagtta 840
Db 781 tcagcggagctgcgaattcccgctccgactggctccgcaaaatattcgaacggcaagtta 840
Qy 841 tggacttgaacataaactccacggtattgagcaggacctatttgagagactcatctcat 900
Db 841 tggacttgaacataaactccacggtattgagcaggacctatttgagagactcatctcat 900
Qy 901 ggagcttcagaatgtggttgcagcaaaccaatgacgaataatccatcacatgacggacgt 960
Db 901 ggagcttcagaatgtggttgcagcaaaccaatgacgaataatccatcacatgacggacgt 960
Qy 961 ccaagtggtgagcgaacaaacaggaagcgcctattcttcagagctgtagctccacac 1020
Db 961 ccaagtggtgagcgaacaaacaggaagcgcctattcttcagagctgtagctccacac 1020
Qy 1021 cggattccggcaactacgttgttggcagggttcgcgctattagagatattgttaggcaag 1080
Db 1021 cggattccggcaactacgttgttggcagggttcgcgctattagagatattgttaggcaag 1080
Qy 1081 accattctgcaactcgtacattacagagttgttttttttttttttttttttttttttt 1140
Db 1081 accattctgcaactcgtacattacagagttgttttttttttttttttttttttttttt 1140
Qy 1141 ctggttgagtgagctcatattctacatcgtatggtctctcaacgctggttccctgcat 1200
Db 1141 ctggttgagtgagctcatattctacatcgtatggtctctcaacgctggttccctgcat 1200
Qy 1201 ctgatatccgctcatttgatccagtcgagcgcctccgctccagtcctcagtgatgca 1260
Db 1201 ctgatatccgctcatttgatccagtcgagcgcctccgctccagtcctcagtgatgca 1260
Qy 1261 tgcacgccaaaattggttgggtggtggtggtggtggtggtggtggtggtggtggtggt 1320
Db 1261 tgcacgccaaaattggttgggtggtggtggtggtggtggtggtggtggtggtggtggt 1320
Qy 1321 gaggttgggggtctccgagcagtgatggtggtgagcgttgggtggtggtggtggtggtggt 1380
Db 1321 gaggttgggggtctccgagcagtgatggtggtgagcgttgggtggtggtggtggtggtggt 1380
Qy 1381 ttgatcaatttacttcttcttcaaatctcttggcagaaaacaaattcattagattagaac 1440
Db 1381 ttgatcaatttacttcttcttcaaatctcttggcagaaaacaaattcattagattagaac 1440
Qy 1441 tggaaacacagtgatgagcaggttaagttaagtcagattccacagaggttaactctttaaga 1500
Db 1441 tggaaacacagtgatgagcaggttaagttaagtcagattccacagaggttaactctttaaga 1500
Qy 1501 aataatgaaccccttagactttatatttgaattataaaataaatttaacttttag 1560
Db 1501 aataatgaaccccttagactttatatttgaattataaaataaatttaacttttag 1560

RESULT 2

AAD03028
ID AAD03028 standard; DNA; 3501 BP.
XX
AC AAD03028;
XX
DT 31-MAY-2001 (first entry)
XX
DE Flax 18.6 kDa oleosin protein DNA.
XX
KW Flax; seed-specific promoter; oleosin protein; seed oil; vaccine;
KW protein expression; anticoagulant; cytokine; growth factor; pectinase;
KW interferon; alpha-1-antitrypsin; anti-obesity protein; haemoglobin;
KW serum albumin; insulin; lactoferrin; myoglobin; pulmonary surfactant;
KW alpha amylase; ds.
XX
OS Linum usitatissimum.
XX
FH Key Location/Qualifiers
FT repeat_unit 14..25
FT FT /*tag= a
FT FT /rpt_type= DIRECT
FT FT /note= "R1 direct repeat"
FT FT 80..89
FT FT /*tag= b
FT FT /rpt_type= DIRECT
FT FT /note= "R2 direct repeat"
FT FT 177..186
FT FT /*tag= c
FT FT /rpt_type= DIRECT
FT FT /note= "R3 direct repeat"
FT FT 837..846
FT FT /*tag= d
FT FT /rpt_type= DIRECT
FT FT /note= "R3 direct repeat"
FT FT 1281..1290
FT FT /*tag= e
FT FT /rpt_type= DIRECT

FT	repeat_unit	/note= "R4 direct repeat"	
FT		1342..1351	
FT		/*tag= f	
FT		/rpt_type= DIRECT	
FT	repeat_unit	/note= "R2 direct repeat"	
FT		1427..1438	
FT		/*tag= g	
FT		/rpt_type= DIRECT	
FT	repeat_unit	/note= "R1 direct repeat"	
FT		1477..1486	
FT		/*tag= h	
FT		/rpt_type= DIRECT	
FT	repeat_unit	/note= "R4 direct repeat"	
FT		1591..1600	
FT		/*tag.. i	
FT		/rpt_type= DIRECT	
FT	repeat_unit	/note= "R5 direct repeat"	
FT		1678..1687	
FT		/*tag= j	
FT		/rpt_type= DIRECT	
FT		/note= "R5 direct repeat"	
FT	CDS	1853..2395	
FT		/*tag= k	
FT		/product= "Flax 18.6kDa O	
XX			
PN	WO200116340-A1.		

WO200116340-A1.

08-MAR-2001.

25-AUG-2000: 2000WO-CA00988.

27-AUG-1999: 99US-0151044.

27-OCT-1999; 99US-016172
28-OCT-1999; 99US-016173
29-OCT-1999; 99US-016174
30-OCT-1999; 99US-016175
31-OCT-1999; 99US-016176
01-NOV-1999; 99US-016177
02-NOV-1999; 99US-016178
03-NOV-1999; 99US-016179
04-NOV-1999; 99US-016180
05-NOV-1999; 99US-016181
06-NOV-1999; 99US-016182
07-NOV-1999; 99US-016183
08-NOV-1999; 99US-016184
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24-NOV-1999; 99US-016200
25-NOV-1999; 99US-016201
26-NOV-1999; 99US-016202
27-NOV-1999; 99US-016203
28-NOV-1999; 99US-016204
29-NOV-1999; 99US-016205
30-NOV-1999; 99US-016206
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02-DEC-1999; 99US-016208
03-DEC-1999; 99US-016209
04-DEC-1999; 99US-016210
05-DEC-1999; 99US-016211
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16-DEC-1999; 99US-016222
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29-DEC-1999; 99US-016235
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01-JAN-2000; 99US-016238
02-JAN-2000; 99US-016239
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24-JAN-2000; 99US-016261
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27-JAN-2000; 99US-016264
28-JAN-2000; 99US-016265
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01-FEB-2000; 99US-016269
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03-FEB-2000; 99US-016271
04-FEB-2000; 99US-016272
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06-FEB-2000; 99US-016274
07-FEB-2000; 99US-016275
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11-FEB-2000; 99US-016279
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13-FEB-2000; 99US-016281
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18-FEB-2000; 99US-016286
19-FEB-2000; 99US-016287
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22-FEB-2000; 99US-016290
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24-FEB-2000; 99US-016292
25-FEB-2000; 99US-016293
26-FEB-2000; 99US-016294
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28-FEB-2000; 99US-016296
29-FEB-2000; 99US-016297
01-MAR-2000; 99US-016298
02-MAR-2000; 99US-016299
03-MAR-2000; 99US-016300
04-MAR-2000; 99US-016301
05-MAR-2000; 99US-016302
06-MAR-2000; 99US-016303
07-MAR-2000; 99US-016304
08-MAR-2000; 99US-016305
09-MAR-2000; 99US-016306
10-MAR-2000; 99US-016307
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19-MAR-2000; 99US-016316
20-MAR-2000; 99US-016317
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22-MAR-2000; 99US-016319
23-MAR-2000; 99US-016320
24-MAR-2000; 99US-016321
25-MAR-2000; 99US-016322
26-MAR-2000; 99US-016323
27-MAR-2000; 99US-016324
28-MAR-2000; 99US-016325
29-MAR-2000; 99US-016326
30-MAR-2000; 99US-016327
31-MAR-2000; 99US-016328
01-APR-2000; 99US-016329
02-APR-2000; 99US-016330
03-APR-2000; 99US-016331
04-APR-2000; 99US-016332
05-APR-2000; 99US-016333
06-APR-2000; 99US-016334
07-APR-2000; 99US-016335
08-APR-2000; 99US-016336
09-APR-2000; 99US-016337
10-APR-2000; 99US-016338
11-APR-2000; 99US-016339
12-APR-2000; 99US-016340
13-APR-2000; 99US-016341
14-APR-2000; 99US-016342
15-APR-2000; 99US-016343
16-APR-2000; 99US-016344
17-APR-2000; 99US-016345
18-APR-2000; 99US-016346
19-APR-2000; 99US-01634

30-MAY-2000; 2000CA-2310304.

(SEMB-) SEMBIOSYS GENETICS INC.

(SEMS) SEMBIOSIS GENETICS INC.
(CSIR) COMMONWEALTH SCI & IND RES ORG.

Chaudhary S, Van Rooijen G, Moloney MM, Singh S;

WPT: 2001-226693/23

WPI; 2001-2266937
P-PSDB: AAY72900

Expressing non-native genes in flax seeds and seeds of other plant species for altering the seed oil and protein composition in the seeds, comprises using seed-specific promoters obtained from flax -

Claim 14: Fig 2: 68pp; English.

The present sequence is a DNA encoding flax 18.6 kDa oleosin protein. The present invention relates to a method for expressing non-native genes in flax seeds. The method comprises introducing a chimeric nucleic acid construct containing a seed-specific promoter obtained from flax and a nucleic acid which is non-native to the promoter, into a flax plant cell and growing the plant cell into a mature flax plant capable of setting seed, where the nucleic acid is expressed in the seed under the control of the promoter. The seed-specific promoters obtained from flax are useful for modifying the protein, oil or polysaccharide composition of the flax seeds and seeds of other plant species. The promoters facilitate expression of proteins, including sulphur-rich protein that are found in lupinus or Brazil nuts in a seed deficient in sulphurous amino acids, peptides having pharmaceutical value such as anticoagulants, antibodies, vaccines, cytokines, growth factors, interleukins, mammalian proteins, including alpha-1-antitrypsin, anti-obesity proteins, haemoglobin, blood proteins, human serum albumin, insulin, lactoferrin, myoglobin, pulmonary surfactants and proteins of industrial value such as alpha-amylase, arabinase, amyloglucosidase, catalase, cellobiohydrolase, pectinases, phytase, papain and xylanase.

Sequence 3501 BP: 1007 A: 777 C: 781 G: 936 T: 0 other:

Query Match 3.0%: Score 61: DB 22: Length 3501:

Best Local Similarity		49.1%	Pred. No. 2.5e-05:		
Matches	190:	Conservative	0:	Mismatches	195: Indels
523	tcctagagaaaagggaatcgatctctgagtatgaaatcgaagtcgacatttttttca	582			
414	tcccatagtctgcacacttccactatcgatgatttlaaacgtatatacagagtcgactc	473			
583	acgtgtccaatcaatcccaacaagaagcagaagcagagtaatttccactatactaca	642			
474	acatgtcccatcacaccacataataagaacatagtttgggagctttcatatttgaacgg	533			
643	caagtaaatagcttaacgtcatcgatgaataaacaagctcgttccctcaagaagggttttc	702			
534	gattgacgacttgcctctc-tcgataatttaacttttttctctcagctgattgtac	591			
703	acatccataacgaccgcgaagcctcatgaagcatttagggagaaccttttggtctcttc	762			
592	gcattccattcggcttcagagcacatcaaaaggatctctccatcgtagtattgggcgttg	651			
763	tcattggcctttataggttgtagccagagctcgccaattccctcgactcggtctcgcaaa	822			
652	tcgtatgatcagaagcagtcgatgagtttcttaattgtcgagctacaggtccgcaaa	711			
823	tattccgaacggcaagttatggacttgcacccaactccacggtattgacaggacctat	882			
712	aaccgcgaggtatagatcgtagtacccaaaaatcagtttctcgtagcggaaatcaac	771			
883	tgtgaagactcatctcatggagcttca	909			
772	actagadactcacccctaagtcatctca	798			

RESULT 3

ABL34155

ABL34155
ID ABL34155 standard: DNA: 15548 BP.

XX
AC ART.34155:

XX
DT 26-MAR-2002 (first entry)

XX
DE Human immune system associated gene SEQ ID NO: 2128.

XX	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	anliarteriosclerotic; anti anaemic; cytostatic; nootropic;
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;
KW	antirheumatic; antiarthritic; antiidiabetic; antipsoriatic;
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW	gene; ds.

XX Homo sapiens.

XX
DN
W0300300938-A2

XX
03-TAM-3003[illegible]

XX

PR 30-JUN-2000; 2000DE-1032329.
PR 01-SEP-2000; 2000DE-1043826.

XX
PA (EPIG-) EPIGENOMICS AG.

XX
PI Olek A. Pienenbrock C. Berlin K:

XX
DB WPT: 2002-130909/17

XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
PT

XX
PS
claim 1: SEO ID NO 2128: 32pp + Sequence Listing: German.

PN WO200200928-A2.
 XX 03-JAN-2002.
 XX 02-JUL-2001; 2001WO-EP07537.
 XX 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-130909/17.
 XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 XX Claim 1; SEQ ID NO 2046; 32pp + Sequence Listing; German.
 XX The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 XX Sequence 40862 BP; 14301 A; 414 C; 7426 G; 18721 T; 0 other;

Query Match 2.5%; Score 51; DB 24; Length 40862;
 Best Local Similarity 46.7%; Pred. NO. 0.027;
 Matches 194; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

QY 1380 attgatacttactcttgccttcaaaattcttggcagaaacaaattcattagattagaa 1439
 DB 21644 ATTAAATTTATATATATATCCCTATTAAATATCCAAATAATAACATTTTATTATAA 21595
 QY 1440 ctggaacacagagtgatgagcggattaaagtcagatccacagaggttacatctcttaag 1499
 DB 21584 TTTTATTTACTATATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 21525
 QY 1500 aaataatgtaaccccttgagacttatatttgcatttaaaaaataatttaactttta 1559
 DB 21524 ATTTAAACCAATTTTTCATTTCTACATATTATATAATAAATAAATAAATAAATAAATAA 21466
 QY 1560 gactttatatagtttttaataactaagtttaaccactctatttttatatogaaactat 1619
 DB 21465 TCTTTTAAAAATATATAATATATACTAATTTTAAATTTATCAATAAATAAATAAATAA 21406
 QY 1620 ttgatgtctcccttgaataaacttggtattgtgtttacagacacctataatcaataaa 1679
 DB 21405 ATTTAATCTTTAAATACAAAATAATTTAAATAATACITATAAATAATTAACCTTAATA 21346
 QY 1680 tcaataactcaactgaagtttgcagtttaattgaaggagattaacggccaatgcaactag 1739
 DB 21345 TACCACATTTCTTTAAATTCATACACTTAAAACTTAAATTTCAATAAATAAATAAATAA 21286
 QY 1740 tatttaacacgaatagattccactagatg9ccattttccatcaataatcagcc 1794
 DB 21285 TCATAATATCTCCCTTAACAATAAANTTACTAANTACATTTTCAAAAACCTTAATACC 21231

RESULT 6
 AAZ37082
 ID AAZ37082 standard; DNA; 1431 BP.
 XX AAZ37082;
 XX 27-MAR-2000 (first entry)

XX DNA sequence encoding a yeast SceI endonuclease.
 DE SceI endonuclease; phosphodiester bond; yeast; genetic engineering;
 KW PCR; polymerase chain reaction; gene cloning; ss.
 XX Saccharomyces cerevisiae.
 XX Key Location/Qualifiers
 FH 1..1431
 FT /tag= a
 FT /product= "SceI endonuclease"
 FT /note= "contains 5 stop codons"
 XX
 XX EP972836-A2.
 XX 19-JAN-2000.
 XX 21-MAY-1999; 99EP-0110008.
 XX 22-MAY-1998; 98JP-0141861.
 XX (RIKA) INST PHYSICAL & CHEM RES.
 PA Morishima N, Shibata T, Mizumura H;
 PI WPI; 2000-099856/09.
 DR P-PSDB; AAY54040.
 XX New modified endonuclease capable of recognizing specific nucleotide
 PT sequence, useful for genetic engineering techniques -
 XX Disclosure; Fig 4; 43pp; English.
 XX The present sequence encodes a yeast SceI endonuclease. The
 CC endonuclease hydrolyses the phosphodiester bond of a polynucleotide
 CC chain. The endonuclease is the 50 kDa subunit of a yeast endonuclease.
 CC The endonuclease gene was modified so that it could be
 CC mass-produced in an expression system such as E. coli or yeast. The
 CC endonuclease polynucleotide sequence was modified by substituting
 CC codons that are unique to mitochondria (the gene is expressed in
 CC mitochondria) with universal codons. The endonuclease cuts molecules
 CC within sequence AA37078, and is therefore useful in genetic engineering
 CC techniques such as PCR (polymerase chain reaction) for cloning,
 CC amplifying and analysing genes.
 XX Sequence 1431 BP; 647 A; 87 C; 103 G; 594 T; 0 other;

Query Match 2.4%; Score 48.6; DB 21; Length 1431;
 Best Local Similarity 54.9%; Pred. NO. 0.026;
 Matches 96; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1515 tttagactttatatatttgcaattaaaaataatttaacttttagactttatatagt 1574
 DB 1223 ttttaacctttacatgataataacaaatttaattataatttaatttagatttaatttata 1282
 QY 1575 tttaataactaagttaaacacactctattttatctatcgaaactatttggatgctccct 1634
 DB 1283 ttaaatcataattgaaataatagagatttggtttagtattctgataataata 1342
 QY 1635 ctataataaacttgattggtttacagacacctataatcaataatcaatactca 1689
 DB 1343 atattaaattgataattgattattattattataataataataataata 1397

RESULT 7
 AAQ24134
 ID AAQ24134 standard; DNA; 1671 BP.
 XX AAQ24134;
 XX 09-NOV-1992 (first entry)

XX DE 50 kD subunit of SclI.
XX KW Endonuclease SclI; PAGE; chromatography; ENS2 gene; ss.
XX OS Saccharomyces cerevisiae.
XX Key Location/Qualifiers
FT CDS 1..1589 /tag= a
FT exon 1..81 /label= SclI_50kD_subunit
FT intron 82..158 /number= 1
FT exon 159..1586 /tag= d
FT intron 159..1586 /number= 2
XX JP04104793-A.
XX 07-APR-1992.
XX 21-AUG-1990; 90JP-0219566.
XX 21-AUG-1990; 90JP-0219566.
XX (RIKA) RIKAGAKU KENKYUSHO.
XX WPI; 1992-164281/20.
XX P-PSDB; AAR22667.
XX ENS2 gene encoding 50kD subunit of SclI endonuclease - used for mass
XX prodn. of recombinant endonuclease in eg. Saccharomyces IAM4274
XX Claim 1; Page 2; 4pp; Japanese.
XX The sequence given encodes the 50kD subunit of endonuclease SclI.
XX Endonuclease SclI can be mass produced from the 50kD subunits
XX expressed from the ENS2 gene. The 50kD subunit was purified by
XX treating SclI from eg. Saccharomyces IAM4274, and by denaturing the
XX protein and subjecting it to PAGE, or by chromatography on a
XX phosphocellulose column.
XX Sequence 1671 BP; 769 A; 108 C; 113 G; 681 T; 0 other;
Query Match 2.4%; Score 48.6; DB 13; Length 1671;
Best Local Similarity 54.9%; Pred. No. 0.028;
Matches 96; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1515 tttagacttatatttgcaataaaataaataaacttttaacttttagactttatatagt 1574
DB 1381 tttagacttatatttgcaataaaataaataaacttttaacttttagactttatatagt 1440
QY 1575 tttaataactaaagttttaaccactctattttatatcgaaactattttagtctccct 1634
DB 1441 ttaatacatataattgaaataaataagattttgttttagtattctgaatatcaata 1500
QY 1635 ctaataaacttggtattgttttaacgaacacctataatacaataaactcaactca 1689
DB 1501 atattaaattgataattgattattattattattattattattattattattattata 1555
RESULT 8
ABL33732/c
ID ABL33732 standard; DNA; 5883 BP.
XX ABL33732;
XX 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 1705.
XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antianaemic; cytostatic; neurotropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antiinflammatory; antiarthritic; antidiabetic; antipsoriatic;
XX acute myeloid leukaemia; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
XX gene; ds.
XX Homo sapiens.
XX WO200200928-A2.
XX 03-JAN-2002.
XX 02-JUL-2001; 2001WO-EP07537.
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation
XX Claim 1; SEQ ID NO 1705; 32pp + Sequence Listing; German.
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.
XX Sequence 5883 BP; 1526 A; 80 C; 1224 G; 3053 T; 0 other;
Query Match 2.4%; Score 48.2; DB 24; Length 5883;
Best Local Similarity 49.3%; Pred. No. 0.06;
Matches 180; Conservative 0; Mismatches 183; Indels 2; Gaps 2;
QY 1422 caattcattagattagaactggaaaccagagtgatgagcggattaaagtcagattccaac 1481
DB 1257 CCATTTAATAATAATTTTAAATAAATAAATAATCATACTTATATTTATATAAAT 1198
QY 1482 agagttaactcttaagaataatgtaacccttttagactttatatattlgaataaa 1541
DB 1197 AATTAAATATTATATAAACAATTTAAACAATCAATTTAAATTTAACTTTAAACTAA 1138
QY 1542 aaaaataatttaacttttagact-ttatatatagttttaaactaaacttaaccactcta 1600
DB 1137 TAAATAATAAATTTTATATAATCTTAATTAATAATATATATACATAAATCAATCTTAC 1078
QY 1601 ttatttatcgaaac-tattttagtctctccctctaaataaacttggtattgttta 1659
DB 1077 ATAAAACTTCAATTCACATAATAACTTTTTTCTTTTAAACAAATCTTACTCTATTA 1018
QY 1660 cagaacctataatacaataactcaactgaactgaatttgcagtttaataaggaat 1719
DB 1017 CCCAACTTAAATACATAATAAATCTCAACCACTCTACCTCTCTCTCTCTCTCTCTCT 958
QY 1720 taacggccaaatgcacttagtattatcaacgaatagattacactagatggccattcc 1779

Db	1174	AAATTTTATATATAATTTAAAGATTCAAACTCTAAATTCAAACTTATAATTCACCAACGTT	1115
Qy	1695	agtttgcggttaattgaagggtataacggcccaaatgcact	1737
Db	1114	TATAACTACCTAAATAATTCATAAATAAATTTACTAAACCTCAT	1072

RESULT	13	
ABL32050/c		
ID	ABL32050 standard; DNA; 16545 BP.	
XX		
XX		
AC	ABL32050;	
DT	26-MAR-2002 (first entry)	
XX		
XX	Human immune system associated gene SEQ ID NO: 23.	
DE		
XX		
XX	Human; immune system disease: cytosine methylation; antiasthmatic;	
KW	antiarteriosclerotic; antitanaemic; cytostatic; nontropic;	
KW	neuroprotective; anti-hiv; anticonvulsant; ophthalmological;	
KW	antipneumatic; antitarrific; antidiabetic; antipsoriatic;	
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;	
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;	
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;	
KW	gene; ds.	

Qy	1614	aactatttgatgctctccctctaaataaaacttggtattgtgtttacagaacctataatc	1675
Db	236	ATTTATTTTATTATTTTATTTTAAACGATATACACCTCTACTACCCAACTAAATA	177
Qy	1674	aaataatcaatactcaactga	1694
Db	176	CAATAATACAAATCTCGACTCA	156

RESULT	14
AAQ24835	
ID	AAQ24835 standard; DNA; 532 BP.
XX	
AC	
XX	AAQ24835;
XX	
DT	25-NOV-1992 (first entry)
XX	
DE	Peroxidase isozyme gene fragment.
XX	
KW	Promoter activity; expression vector; ss.
XX	
OS	Armoracia rusticana.
XX	
PN	JP04126088-A.
XX	
PD	27-APR-1992.
XX	
PF	14-SEP-1990; 90JP-0244779.
XX	
PR	14-SEP-1990; 90JP-0244779.
XX	
PA	(TOYM) TOYOBO KK.
XX	
DR	WPI; 1992-189675/23.
XX	
PT	DNA fragment with good promoter activity in plant cells - used
PT	for expression vector of various kinds of foreign gene
XX	
PS	Claim 1; Page 1; 7pp; Japanese.
XX	
CC	The sequence given is a DNA fragment which has promoter activity;
CC	It is derived from the peroxidase isozyme gene and has strong
CC	promoter activity in plants and yeast. This sequence can be used
CC	expression vectors for various kinds of foreign genes eg. beta-
CC	glucuronidase, peroxidase, ascorbate oxidase and luciferase.
XX	
SQ	Sequence 532 BP; 210 A; 71 C; 58 G; 193 T; 0 other;

RESULT 15
AAZ98840
ID AAZ98840 standard: DNA: 532 BP.

```

XX AA298840;
AC
XX 20-JUN-2000 (first entry)
XX
XX DE Horseradish peroxidase isozyme gene promoter fragment.
XX
XX KW Horseradish peroxidase; isozyme; promoter activity; transgenic plant; ss.
XX
XX OS Armoracia rusticana.
XX
XX PN JP2000041688-A.
XX
XX PD 15-FEB-2000.
XX
XX PF 14-SEP-1990; 99JP-0196728.
XX
XX PR 14-SEP-1990; 90JP-0244779.
XX
XX PA (TOYM ) TOYOB0 KK.
XX
XX DR WPI; 2000-295783/26.
XX
XX PT A DNA fragment, from horseradish peroxidase isozyme gene, having
XX promoter activity - useful in an expression vector which can express
XX various heterogenes
XX
XX Example 1; Page 6; 7pp; Japanese.
XX
XX This sequence represents a DNA fragment of the horseradish peroxidase
XX isozyme gene. The fragment has promoter activity. The invention relates
XX to a DNA fragment derived from the horseradish peroxidase isozyme gene.
XX The fragment can be inserted into a vector, which when expressed in a
XX plant cell exhibits promoter activity. The promoter activity is at least
XX 4 times higher than the cauliflower mosaic virus 35S promoter. An
XX expression vector containing the DNA fragment can be used to transform
XX CC plants and cause the expression of heterogenes.
XX
XX SQ Sequence 532 BP; 210 A; 71 C; 58 G; 193 T; 0 other;

```

```

Query Match      2.3%; Score 47.2; DB 21; Length 532;
Best Local Similarity 57.1%; Pred. No. 0.039;
Matches 105; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 1515 tttagactttatatatttgc-aattaaaaaaataatttaacttttagactttatatatag 1573
    ||||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 ttataataatagtgattgcaaatgtgcataagaagaattcattagtaacctttatttatcg 116

QY 1574 tttaataactaagtttaaccactctattttatatatcgaactatttgatgctcccc 1633
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 117 tgaataatttttttctaaataattaaattttaagttgaaactacaaattataaaaaat 176

QY 1634 tctaaataaacttggtattgttttacagaacctataatcaataatcaatactcaactg 1693
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 acaaatggaattataatgtatttccaaggtacataaagaagaagaattcttattataaac 236

QY 1694 aagt 1697
    |||
Db 237 acgt 240

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Search completed: August 25, 2002, 17:21:01
 Job time: 14769 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 13:11:16 ; Search time 133.71 Seconds
(without alignments)
9183.471 Million cell updates/sec

Title: US-09-645-593-8

Perfect score: 4999

Sequence: 1 ctcaagcatacggacaagg.....tcnattgtanattgncgttg 4999

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/6C_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	129.6	2.6	3113	1	US-08-146-422-20
2	129.6	2.6	3113	1	US-08-626-554-2
3	102.4	2.0	1685	1	US-08-486-721A-1
4	101.2	2.0	1556	1	US-08-486-721A-2
5	68.8	1.4	7218	1	US-08-232-463-14
6	61.2	1.2	7218	1	US-08-232-463-14
7	47.4	0.9	1240	1	US-08-142-393-2
8	45.4	0.9	1431	4	US-09-316-083-2
9	43.8	0.9	8920	2	US-08-446-855A-1
10	43.8	0.9	8920	4	US-09-150-741-1
11	43.4	0.9	5923	4	US-09-064-922-3
12	42.4	0.8	3319	2	US-08-960-022-19
13	42.2	0.8	663	4	US-08-998-416-191
14	42	0.8	854	4	US-08-998-416-534
15	41.6	0.8	68750	3	US-09-335-409-1
16	41.6	0.8	68750	4	US-09-568-102-1
17	41.6	0.8	68750	4	US-09-567-969-1
18	41.6	0.8	68750	4	US-09-568-480-1
19	41.6	0.8	68750	4	US-09-568-486-1
20	41.6	0.8	68750	4	US-09-568-472-1
21	41.4	0.8	662	4	US-08-998-416-185
22	41.4	0.8	665	4	US-08-998-416-937
23	41.4	0.8	701	4	US-08-998-416-701
24	41.4	0.8	711	4	US-08-998-416-786
25	41.4	0.8	724	4	US-08-998-416-683
26	41.4	0.8	732	4	US-08-998-416-1036
27	41.4	0.8	828	4	US-08-998-416-538

C 28	41.4	0.8	834	4	US-08-998-416-305	Sequence 305, Appl
29	41.4	0.8	860	4	US-08-998-416-287	Sequence 287, Appl
30	40.4	0.8	289	4	US-09-007-005-17	Sequence 17, Appl
31	40.4	0.8	289	4	US-09-244-796-17	Sequence 17, Appl
32	40.4	0.8	636	4	US-08-998-416-1137	Sequence 1137, Appl
33	40.4	0.8	837	4	US-08-998-416-288	Sequence 288, Appl
C 34	40.2	0.8	5495	1	US-08-602-010A-1	Sequence 1, Appl
35	40.2	0.8	5495	1	US-08-602-010A-2	Sequence 2, Appl
C 36	40.2	0.8	5495	1	US-08-680-726A-1	Sequence 1, Appl
37	40.2	0.8	5495	1	US-08-680-726A-2	Sequence 2, Appl
C 38	40.2	0.8	5495	3	US-09-092-409-1	Sequence 1, Appl
39	40.2	0.8	5495	3	US-09-092-409-2	Sequence 2, Appl
C 40	40.2	0.8	10592	1	US-08-680-726A-51	Sequence 51, Appl
41	40.2	0.8	10592	1	US-08-680-726A-52	Sequence 52, Appl
C 42	40.2	0.8	10592	3	US-09-092-409-51	Sequence 51, Appl
43	40.2	0.8	10592	3	US-09-092-409-52	Sequence 52, Appl
C 44	39.6	0.8	1125	4	US-09-516-914-12	Sequence 12, Appl
45	39.6	0.8	1298	1	US-08-473-157A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-146-422-20
; Sequence 20 Application US/08146422
; Patent No. 5543576
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRILJ
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146.422
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/POCKET NUMBER: 44615-20011.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-146-422-20

Query Match 2.6%; Score 129.6; DB 1; Length 3113;
Best Local Similarity 55.0%; Pred. No. 2.8e-27;

QY 4153 atactaatactattattataaacta 4179
|||||
Db 8533 ATATATATATATATATATATATATTA 8507

RESULT 11
US-09-064-922-3/c
; Sequence 3, Application US/09064922
; Patent No. 6222095
; GENERAL INFORMATION:
; APPLICANT: Callis, Judy
; APPLICANT: Worley, Cathy K.
; TITLE OF INVENTION: Sequences from Auxin-Induced Gene
; TITLE OF INVENTION: Products Targeting Fusion Proteins for Degradation
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,922
; FILING DATE: 22-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hyman, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 023070-08540005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5923 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(2667..3012, 4327..4420, 4778..4877)
; OTHER INFORMATION: /product= "PSIA6 auxin-induced"
; OTHER INFORMATION: /protein= "gene for PS-IAA6 (indoleacetic
; OTHER INFORMATION: /note= "acid-inducible gene of pea
; OTHER INFORMATION: (Pisum sativum)"
US-09-064-922-3

Query Match 0.9%; Score 43.4; DB 4; Length 5923;
Best Local Similarity 53.9%; Pred. No. 0.084; 76; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 0;
QY 1488 acatctcttaagaataatgttaaccccttagactttatatttgcaattaaaaaata 1547
|||||
Db 5400 ATATCTATAATAATTTATTTATTTTCCCTTTATTTTAAATTTACTTTATTTTAAATA 5341
QY 1548 atttaacttttagactttatatttgatttaataactaagttaaaccactctattatta 1607
|||||
Db 5340 AAATATTCTTTATTTATTTATGCGCAATTTTAAATAATAGAAATAAACCTCTATATTTCCTA 5281
QY 1608 tategaactatttgtagtctccctctctaaataaaacttgggtatt 1652
|||||
Db 5280 AAAGGCAATATATAGTTTACATACATACATTTTAAACACATGGTGT 5236

RESULT 12
US-08-960-022-19/c
; Sequence 19, Application US/08960022
; Patent No. 5978837
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,022
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3319 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-960-022-19
Query Match 0.8%; Score 42.4; DB 2; Length 3319;
Best Local Similarity 52.9%; Pred. No. 0.11;
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 3926 ttgttggtttttatgtttttttaaatacatgaatttttaatttttaataataatctcc 3985
|||||
Db 3318 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTCC 3259
QY 3986 aatcggagaacaacattccatccatccatggatgttttttaaccccaaatctagtcttgag 4045
|||||
Db 3258 AAATACAAACATGGGATTTTCAAAAGTGGATTTTCTTATATATATATATATATATCTGCTG 3199
QY 4046 agatgaagcatcacccgacagctgttcgaactatccctcaaaagcttttaaaa 4097
|||||
Db 3198 CAACAGTGGATCAAAAGACAGAGAGTGTCTTAGCATGATTCTTTGAAA 3147
RESULT 13
US-08-998-416-191
; Sequence 191, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer

APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1076UP
US-08-998-416-191

Query Match 0.8%; Score 42.2; DB 4; Length 663;
Best Local Similarity 49.4%; Pred. No. 0.037;
Matches 132; Conservative 2; Mismatches 130; Indels 3; Gaps 1;
QY 1380 attgatacaattactcttcttgcctcaattcttggcagaaacaaattcattagattagaa 1439
DB 219 ATTATTAGATTAAAGTATCTTAAATAATATATTATTAGGTAATAATATTAGTAGGTAGTAA 278
QY 1440 ctggaacacagagtgatgagcggattagtcagattccaaacagagttacatctcttaag 1499
DB 279 TATCCAAATTARRGGGTAGACTATTAAATAGAAATATTATTAGACTAAATAAATAATAT 338
QY 1500 aaataatgtaacccctttagactttatatttgcgaattaaataaaataaacttta 1559
DB 339 TATGAAGGTACATTAAATAATTATATATAT---CAATGAAGTAATTAATAATTATATA 395
QY 1560 gactttatatagttttaataactagtttaaccactctattatttatatcgaaactat 1619
DB 396 TAAATTAATTAATATACACTTAATTAATAAACTTAATAATCTATTATTATTAATAAAAA 455
QY 1620 ttgtatgtctccctctcaataaactt 1646
DB 456 TGGTATATTAATTAATAATTAATTAAT 482

RESULT 14
US-08-998-416-534

Sequence 534, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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INFORMATION FOR SEQ ID NO: 534:
SEQUENCE CHARACTERISTICS:
LENGTH: 854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1372UP
US-08-998-416-534

Query Match 0.8%; Score 42; DB 4; Length 854;
Best Local Similarity 48.7%; Pred. No. 0.051;
Matches 145; Conservative 0; Mismatches 150; Indels 3; Gaps 1;
QY 1380 attgatacaattactcttcttgcctcaattcttggcagaaacaaattcattagattagaa 1439
DB 219 ATTATTAGATTAAAGTATCTTAAATAATATATTATTAGGTAATAATATTAGTAGGTAGTAA 278
QY 1440 ctggaacacagagtgatgagcggattagtcagattccaaacagagttacatctcttaag 1499
DB 279 TATCCAAATTAAAGGTAGACTATTAAATAGAAATATTATTAGACTAAATAAATAATAT 338
QY 1500 aaataatgtaaccccttttagactttatatttgcgaattaaataaaataaacttta 1559
DB 339 TATGAAGGTACATTAAATAATTATATATAT---CAATGAAGTAATTAATAATTATATA 395
QY 1560 gactttatatagttttaataactagtttaaccactctattatttatatcgaaactat 1619
DB 396 TAAATTAATTAATATACACTTAATTAATAAACTTAATAATCTATTATTATTAATAAAAA 455
QY 1620 ttgtatgtctccctctcaataaacttggattgttttacagaaactataatcaaat 1677

